

FIG. 1A

1	CCCACGCGTCCGATTAAAGTGAGGAGAGAGCTACAACCAAGTAAGCAAGTGTCAGGGGCTC	60
61	ACCAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTC	120
1	<u>M O G Q G R R R G T C K D I F C S K</u>	18
121	AATGGCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTG	180
19	<u>M A S Y L Y G V L F A V G L C A P I Y C</u>	38
181	TGTGTCCCCGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCACCCC	240
39	V S P A N A P S A Y P R P S S T K S T P	58
241	TGCCTCACAGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGT	300
59	A S Q V Y S L N T D F A F R L Y R R L V	78
301	TTTGGAGACCCCGAGTCAGAACATCTTCTCTCCCCTGTGAGTGTCTCCACTTCCCTGGC	360
79	L E T P S Q N I F F S P V S V S T S L A	98
361	CATGCTCTCCCTTGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTT	420
99	M L S L G A H S V T K T Q I L Q G L G F	118
421	CAACCTCACACACACACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTC	480
119	N L T H T P E S A I H Q G F Q H L V H S	138
481	ACTGACTGTTCCCAGCAAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAA	540
139	L T V P S K D L T L K M G S A L F V K K	158
541	GGAGCTGCAGCTGCAGGCAAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGT	600
159	E L Q L Q A N F L G N V K R L Y E A E V	178
601	CTTTTCTACAGATTTCTCCAACCCCTCCATTGCCAGGCGAGGATCAACAGCCATGTGAA	660
179	F S T D F S N P S I A Q A R I N S H V K	198
661	AAAGAAGACCCAAGGGAAGGTTGTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCAT	720
199	K K T Q G K V V D I I Q G L D L L T A M	218
721	GGTTCTGGTGAATCACATTTTCTTTAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATA	780
219	V L V N H I F F K A K W E K P F H L E Y	238
781	TACAAGAAAGAACTTCCCATTCCTGGTGGGCGAGCAGGTCACTGTGCAAGTCCCCATGAT	840
239	T R K N F P F L V G E Q V T V Q V P M M	258
841	GCACCAGAAAGAGCAGTTCGCTTTTGGGGTGGATACAGAGCTGAACTGCTTTGTGCTGCA	900
259	H Q K E Q F A F G V D T E L N C F V L Q	278

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FIG. 2

	1	50
AL132708_FL	(1) MQGQRRRGTCCKDIFCSKMASYLYGVFAVGLCAPIYCVSPANAPSAYPR	
AACT_HUMAN	(1) -----MERMLPLALGLLAAGFCPAVLCHPNSPLD	
KAIN_HUMAN	(1) -----MHLIDYLLELLVGLLALSHGQLHVEHDGESCS	
THBG_HUMAN	(1) -----MSPFLYLVLVLGLHATIHCAASPEGKVTACHS	
	51	100
AL132708_FL	(51) PS-----STKSTPASQVYSLNTDEAFRLYRRLVLETSPQNIFESPVS	
AACT_HUMAN	(31) EENLTQENQDRGTHVDLGLASANVDAFSLYKQLVLKAPDKNVIESPLSI	
KAIN_HUMAN	(33) NSSHQIILETGEGSPSLKIAPANADAFRFYLIASETPGKNIFESPLSI	
THBG_HUMAN	(33) -----SQPNATLYKMSSINADAFNLRYRFTVETPDKNIFESPVSI	
	101	150
AL132708_FL	(94) STSLAMISLGAHSVTKQTILQGLGFNLHTHPESAIHQGFQHLVHSETVPS	
AACT_HUMAN	(81) STALAFSLGAHNTTLTEILKGLKFNLTETSEAEIHQSFOHLLRTINQSS	
KAIN_HUMAN	(83) SAAYAMISLGACSHSRSQILEGLGFNLTELSSESDVHRGFQHLHTINLPG	
THBG_HUMAN	(74) SAALVMSLFGACCSQTQTEIVETLGFNLTDTPMVEIQHGFQHLICSLNFPK	
	151	200
AL132708_FL	(144) KDETLKMGSALFVKKEQLQANFLGNVKRLYEAEVFSTDESNPISIAQART	
AACT_HUMAN	(131) DELQLSMGNAMFVKEQLSLDRFTEDAKRLYGSEAFATDFQDSAAAKKLI	
KAIN_HUMAN	(133) HGLETRVGSALFLSHNLKFLAKFLNDTMAVYEAKLFHTNFYDVTGTIQLI	
THBG_HUMAN	(124) KELELQIGNALEFIGKHLKPLAKFLNDVKTLYETEVEFSTDESNISAAKQEI	
	201	250
AL132708_FL	(194) NSHVKKKTQCKVVDIIQGLDLLTAMVLVNHIFKAKWEKPFHLEYTRKNF	
AACT_HUMAN	(181) NDYVKNGTGKITDLIKDLSQTMVLVNYIFKAKWEMPFDPQDTHQSR	
KAIN_HUMAN	(183) NDHVKKETRGKIVDLVSELKKDVLMLVNYTYFKALWEKPFISSRTTPKD	
THBG_HUMAN	(174) NSHVEMQTKGKVGLIQDLKPNTIMVLVNYIHFKAQWANPFDPSTEDSS	
	251	300
AL132708_FL	(244) PFLVGEQVTVQVPMMHQKEQFAFGVDTELNCFVLQMDYKGDVAFFVIPS	
AACT_HUMAN	(231) FYLSKKKWVMVPMMSLHHLTIPYFRDEELSCTVVELKYTGNASALEIIPD	
KAIN_HUMAN	(233) FYVDENTTVRVPMMLQDQEHHWYLDHRYLPCSVLRMDYKGDATVFVILPN	
THBG_HUMAN	(224) SFLIDKTTTVQVPMMHQMEQYHYLVDMEINCTVLQMDYKSNALALEVLPK	
	301	350
AL132708_FL	(294) KGKMRQLEQALSARTLIKWSHSLQKR---WIEVFIPRFESISASYNLETI	
AACT_HUMAN	(281) QDKMEEVEAMLLPETLKRWRDSLEFR---EIGELYLPKFSISRDNINDI	
KAIN_HUMAN	(283) QGKMREIEEVLTPPEMLMRWNNLLRKRNFYKKLELHLPKFSISGSYVLDQI	
THBG_HUMAN	(274) EGQMESVEAAMSSKTLKKWNRLQKG---WVDLFVPKFSISATYDLGAT	
	351	400
AL132708_FL	(340) LPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT	
AACT_HUMAN	(328) ELQLGIEEAFTSKADLSGITGARNLAVSQVHKAVLDVFEEGTEASAATA	
KAIN_HUMAN	(333) LPRLGFTDLFSKWADLSGITKQOKLEASKSFHKATLDVDEAGTEAAAATT	
THBG_HUMAN	(320) LLKMGIQHAYSENADFSLTEDNGLKLSNAAHKAVLHIGKGTAAAVPE	
	401	446
AL132708_FL	(390) TKFIVRSKDGPSYFTVSNRTEFLMMTNKATDGILFLGKVENPTKS	
AACT_HUMAN	(378) VKITLLSALVETRRTIVRFNRPELMIIVPTDTQNIFFMSKVTNPKQA	
KAIN_HUMAN	(383) FAIKFFSAQTN-RHILRFNRPELVVIFSTSTQSVLEFLGKVVDETKP	
THBG_HUMAN	(370) VELSDQPENTFLHPIIQIDRSFMLLILERSTRSILFLGKVVNPTKA	

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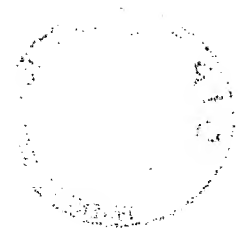


FIG. 3

LSI-01 pdblqlp	MOGQGRRRGT CKDIFCSKMA SYLYGVLFV GLCPIYCVS PANAPSAYPR MDPQ GDAAQKTDTS
LSI-01 pdblqlp	PSSTKSTPAS QVYSLNTDFA FRLYRRLVLE TPSQNLFFSP VSVSESLAME HHDQDHPTFN KITPNLAERA FSLYRQAAHQ SNSTNRRFSP VSIAMAFAM
LSI-01 pdblqlp	SLGAHSVTKT QELQEGFNL THTDESATHQ GQGHVHSET VESKDETHKM SEGTKADTHD ETEEGENFNL TEIPRAQHEH GEGEMLRTEN QPDSQEQHTT
LSI-01 pdblqlp	GSALFVKKEL QLQANFLGNV KRLYEAHVFS TDESNPISIAQ ARENSHVKKK GNGLFLSEGL KLVDKELIEDV KKLHSEAFV VNEGDTEAK KQNDYMEKG
LSI-01 pdblqlp	TQKVVVDIIQ GLDLLTAMVL VNHFFRAKW EKPFLLEYTR KNFPFLVGEQ TQKIVDLVK ELDRTIVFAL VNYFFRGKW ERPFVVKDT. EEEDFHVQV
LSI-01 pdblqlp	VTQVQPMHQ KEQFAGVDT ELNCFVLQMD YKGDVAFFV LPSKGMROE TVKVPMMKR LGMFNIOHCK KLSWVLLMK YLGNATAIFF LPDEGLQHL
LSI-01 pdblqlp	EQALSARTLI KWSHSLQKW IEVFIPRFSI SASYNLETIL PKMGTQNAED ENELTHDIIT KPLENEDRRS ASLHLPKLSI TGTIDEKSVL GQLGITKVS
LSI-01 pdblqlp	KNADFSGIK RDSLQVSKAT HKAVIDVSEE GTEATAATTT KFEVRSKGGP NGADLSGVTE EAPKLSKAV HKAVIDIDEK GTEAAGAMFL EATFMSI..P
LSI-01 pdblqlp	S.YFTVSFNR TFLMMITNKA TDGILFLGKV ENPTKS PE...VKFNK PFVFLMIEQN TKSPFLMGKV VNPTOK

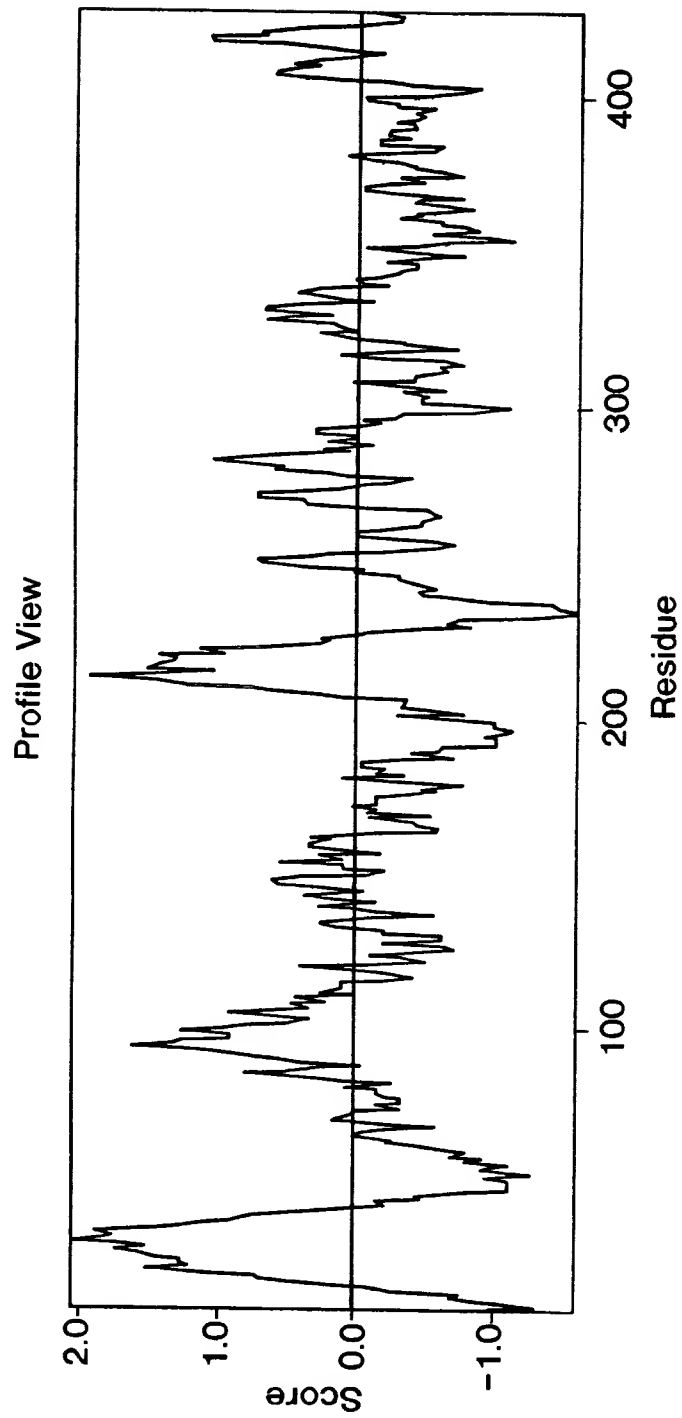
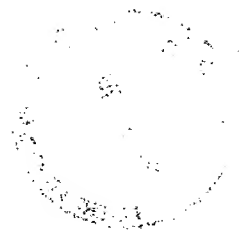


FIG. 4



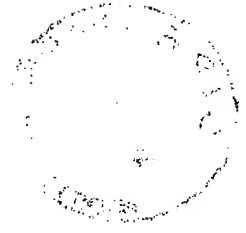


FIG. 5A

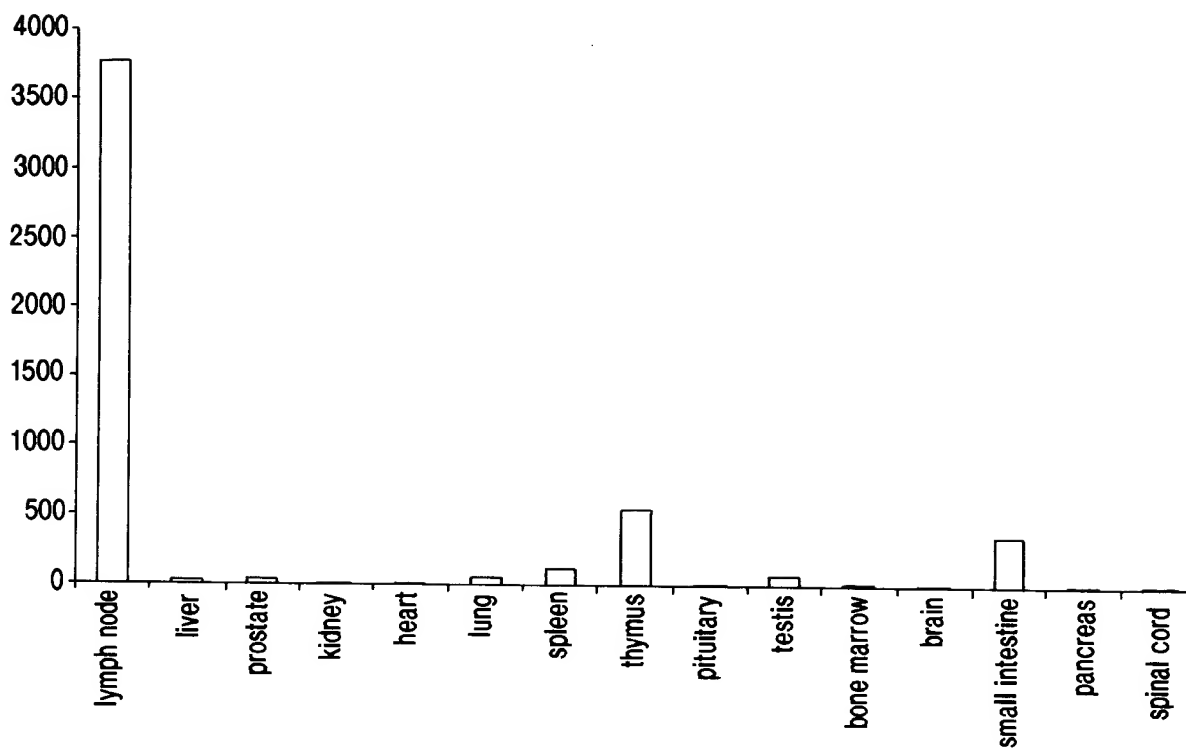
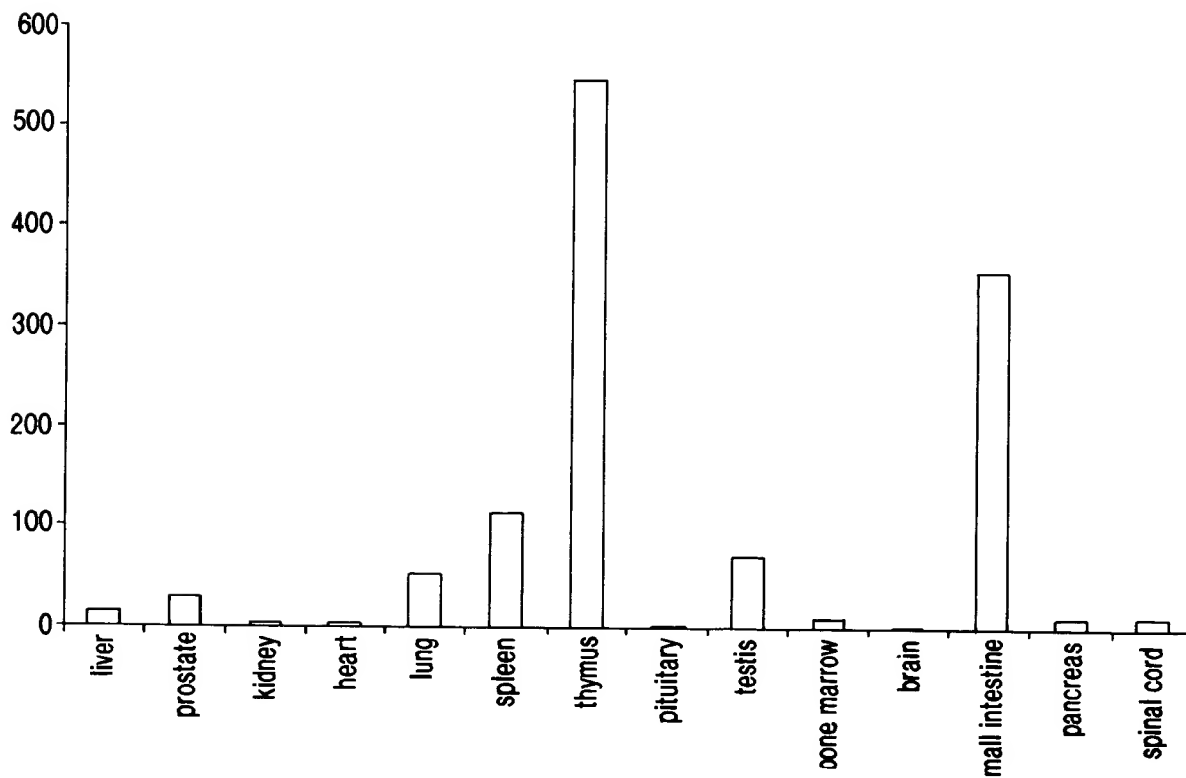


FIG. 5B



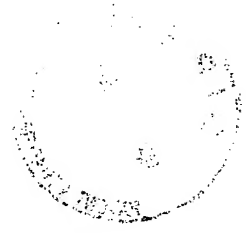


FIG. 6

Protein	Genbank ID	Identities	Similarities
human α_1 -antichymotrypsin	gi 112874	46%	52%
human Kallistatin	gi 5453888	48%	56%
human thyroxin-binding globulin	gi 37142	51%	57%
human α_1 -antithrypsin	gi 6137432	43%	50%

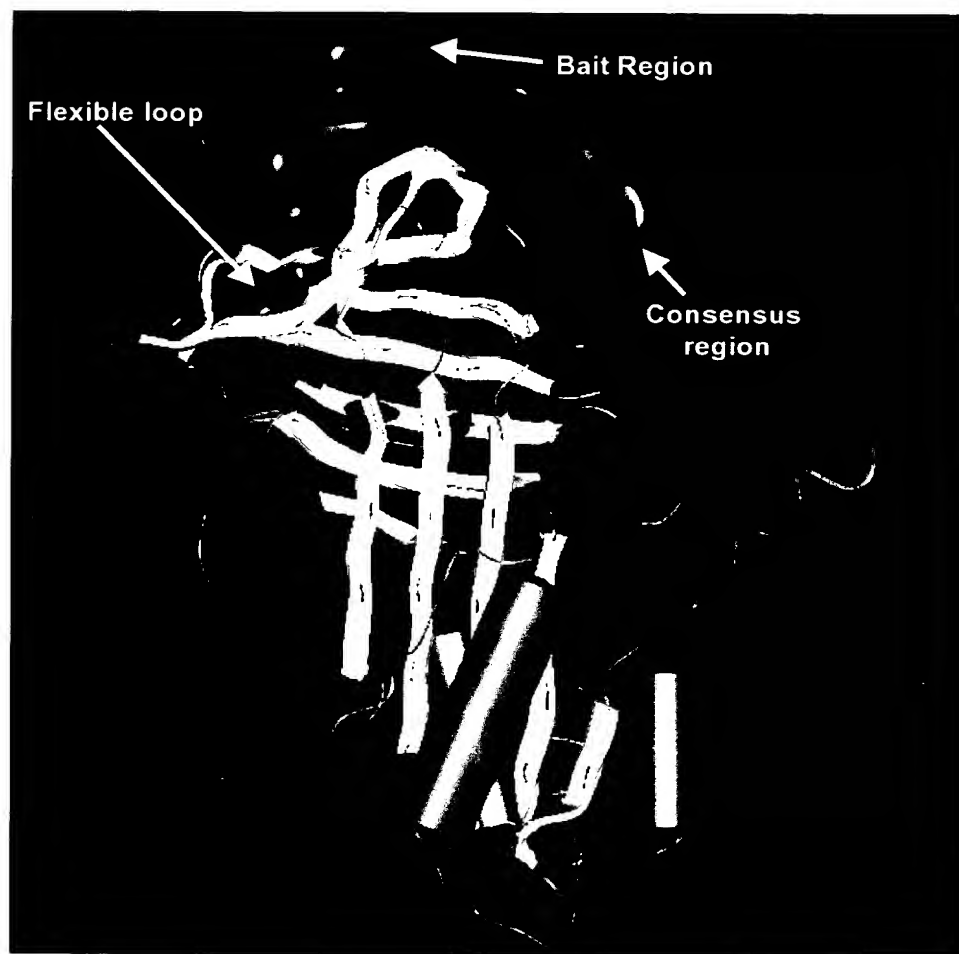


FIG. 7